

RAW SEQUENCE LISTING

DATE: 06/14/2001

PATENT APPLICATION: US/09/742,454A

TIME: 11:01:20

Input Set : A:\Pto.amc

Output Set: N:\CRF3\06142001\I742454A.raw

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3 <110> APPLICANT: WILEY, Steven R.
5 <120> TITLE OF INVENTION: TWEAK Receptor
7 <130> FILE REFERENCE: 2968-B
9 <140> CURRENT APPLICATION NUMBER: US/09/742,454A
10 <141> CURRENT FILING DATE: 2000-12-19
12 <150> PRIOR APPLICATION NUMBER: 60/172,878
13 <151> PRIOR FILING DATE: 1999-12-20
15 <150> PRIOR APPLICATION NUMBER: 60/203,347
16 <151> PRIOR FILING DATE: 2000-05-10
18 <160> NUMBER OF SEQ ID NOS: 7
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 898
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (52)..(873)
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
33 fusion protein construct
35 <400> SEQUENCE: 1
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37 Met Ala
38 1
40 aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
41 Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
42 5 10 15
44 ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
45 Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
46 20 25 30
48 ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
49 Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
50 35 40 45 50
52 aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
53 Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
54 55 60 65
56 agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
57 Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu
58 70 75 80
60 gag ctg gtg gca gag gag gac cag gac ccg tcg gaa ctg aat ccc cag 345
61 Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln
62 85 90 95
64 aca gaa gaa agc cag gat cct gcg cct ttc ctg aac cga cta gtt cgg 393
65 Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg
66 100 105 110
68 cct cgc aga agt gca cct aaa ggc cgg aaa aca cgg gct cga aga gcg 441

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69 Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala
70 115 120 125 130
72 atc gca gcc cat tat gaa gtt cat cca cga cct gga cag gac gga gcg 489
73 Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp Gly Ala
74 135 140 145
76 cag gca ggt gtg gac ggg aca gtg agt ggc tgg gag gaa gcc aga atc 537
77 Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala Arg Ile
78 150 155 160
80 aac agc tcc agc cct ctg cgc tac aac cgc cag atc ggg gag ttt ata 585
81 Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile
82 165 170 175
84 gtc acc cgg gct ggg ctc tac tac ctg tac tgt cag gtg cac ttt gat 633
85 Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp
86 180 185 190
88 gag ggg aag gct gtc tac ctg aag ctg gac ttg ctg gtg gat ggt gtg 681
89 Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp Gly Val
90 195 200 205 210
92 ctg gcc ctg cgc tgc ctg gag gaa ttc tca gcc act gcg gcc agt tcc 729
93 Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser
94 215 220 225
96 ctc ggg ccc cag ctc cgc ctc tgc cag gtg tct ggg ctg ttg gcc ctg 777
97 Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu Ala Leu
98 230 235 240
100 cgg cca ggg tcc tcc ctg cgg atc cgc acc ctc ccc tgg gcc cat ctc 825
101 Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala His Leu
102 245 250 255
104 aag gct gcc ccc ttc ctc acc tac ttc gga ctc ttc cag gtt cac tga 873
105 Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val His
106 260 265 270
108 gcggccgcgg atctgttttaa actag 898
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112 <211> LENGTH: 273
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
118 fusion protein construct
120 <400> SEQUENCE: 2
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124 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met
125 20 25 30
127 Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
128 35 40 45
130 Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
131 50 55 60
133 Arg Ser Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala
134 65 70 75 80
136 Gln Glu Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn

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137      85      90      95
139 Pro Gln Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu
140      100      105      110
142 Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg
143      115      120      125
145 Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
146      130      135      140
148 Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala
149 145      150      155      160
151 Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu
152      165      170      175
154 Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
155      180      185      190
157 Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp
158      195      200      205
160 Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
161      210      215      220
163 Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
164 225      230      235      240
166 Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
167      245      250      255
169 His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
170      260      265      270
172 His
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176 <211> LENGTH: 868
177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (53)..(442)
184 <400> SEQUENCE: 3
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186                                     Met Ala
187                                     1
189 cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
190 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
191      5      10      15
193 ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
194 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
195      20      25      30
197 ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
198 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
199 35      40      45      50
201 gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
202 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
203      55      60      65
205 tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
206 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu

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207          70          75          80
209 ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
210 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
211          85          90          95
213 ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
214 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile
215          100          105          110
217 gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
218 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
219 115          120          125
221 caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502
223 cagtctctgc ctcccagacg cggcgggagc caagctcctc caaccacaag gggggtgggg 562
225 ggcggtgaat cacctctgag gcctgggccc aggggttcagg ggaaccttcc aagggtgtctg 622
227 gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctggctca cacaaaacag 682
229 ctgacactga ctaaggaact gcagcatttg cacaggggag gggggtgccc tccttcctag 742
231 aggccctggg ggccaggctg acttgggggg cagacttgac actaggcccc actcactcag 802
233 atgtcctgaa attccaccac gggggtcacc ctgggggggtt agggacctat ttttaacact 862
235 agaggg 868
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239 <211> LENGTH: 129
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 4
244 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
245 1 5 10 15
247 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
248 20 25 30
250 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
251 35 40 45
253 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
254 50 55 60
256 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
257 65 70 75 80
259 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
260 85 90 95
262 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
263 100 105 110
265 Pro Ile Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
266 115 120 125
268 Gln
271 <210> SEQ ID NO: 5
272 <211> LENGTH: 129
273 <212> TYPE: PRT
274 <213> ORGANISM: Mus sp.
276 <400> SEQUENCE: 5
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278 1 5 10 15
280 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly
281 20 25 30

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283 Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
284           35           40           45
286 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
287           50           55           60
289 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
290 65           70           75           80
292 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
293           85           90           95
295 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
296           100          105          110
298 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
299           115          120          125
301 Gln
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 932
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <221> NAME/KEY: CDS
311 <222> LOCATION: (1)..(930)
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
315     receptor fusion protein construct
317 <400> SEQUENCE: 6
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319 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
320 1           5           10          15
322 ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc 96
323 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
324           20           25           30
326 acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag 144
327 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
328           35           40           45
330 tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc 192
331 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
332           50           55           60
334 ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga 240
335 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
336 65           70           75           80
338 tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc 288
339 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
340           85           90           95
342 gag ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc 336
343 Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
344           100          105          110
346 ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg 384
347 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
348           115          120          125
350 agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg 432

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/742,454A

DATE: 06/14/2001

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\06142001\I742454A.raw

L:396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6